



## SEQUENCE LISTING

5	(1) GENE	ERAL INFORMATION:
10	(i)	APPLICANT: Brodeur, Bernard R Martin, Denis Hamel, Josee Rioux, Clement
	(ii)	TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN OF NEISSERIA MENINGITIDIS
15	(iii)	NUMBER OF SEQUENCES: 26
20	(iv)	CORRESPONDENCE ADDRESS:  (A) ADDRESSEE: Goudreau Gage Dubuc & Martineau Walker  (B) STREET: 800 Place Victoria, Suite 3400, Tour de la Eourse  (C) CITY: Montreal  (D) STATE: Quebec  (E) COUNTRY: Canada
25		(F) ZIP: H4Z 1E9
30	(V)	COMPUTER READABLE FORM:  (A) MEDIUM TYPE: Floppy disk  (B) COMPUTER: IBM PC compatible  (C) OPERATING SYSTEM: PC-DOS/MS-DOS  (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
35	(vi)	CURRENT APPLICATION DATA:  (A) APPLICATION NUMBER:  (B) FILING DATE:  (C) CLASSIFICATION:
40	(vii)	PRIOR APPLICATION DATA:  (A) APPLICATION NUMBER: US 08/406.362  (B) FILING DATE: 17-MAR-1995
	(vii)	PRIOR APPLICATION DATA:  (A) APPLICATION NUMBER: US (PROVIS) 60/001,983  (B) FILING DATE: 04-AUG-1995
45	(viii)	ATTORNEY/AGENT INFORMATION:  (A) NAME: Leclerc/Dubuc/Prince, Alain/Jean/Gaetan  (C) REFERENCE/DOCKET NUMBER: BIOVAC-1 PCT
50	(ix)	TELECOMMUNICATION INFORMATION: (A) TELEPHONE: 514-397-7400 (B) TELEFAX: 514-397-4382
55	(2) INFOR	MATION FOR SEQ ID NO:1:
	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 830 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double
60		(D) TOPOLOGY: linear
	(ii)	MOLECULE TYPE: DNA (genomic)



		(111	, nr	POIN	EIIC	AL:	NO				•						
•		(iv	) AN	TI-S	ENSE	: NO											
5		(Vi	(.	A) O	RGAN	OURC ISM: N:(6	Nei	sser )	ia m	enin	giti	dis					
10		(ix		A) N.	AME/	KEY: ION:		66	7				,				
15		(ix		A) N.	AME/	KEY:			tide 9							٠	
20		(ix		A) N	AME/	KEY: ION:			tide 7				•				
		(xi	) SE	QUEN	CE D	ESCR:	IPTI	: : MC	SEQ :	ID N	0:1:						
25	TCG	GCAA	AGC A	AGCC	GGAT	AC C	GCTA(	CGTA:	T CT	TGAA	GTAT	TGA	AAAT	ATI .	ACGA'	TGCAAA	60
	AAA	SAAA	ATT :	raag:	TATA.	AT AC	CAGC	AGGA'	T TC	TTTA	ACGG	ATT	CTTA	ACA .	ATTT	PTCTAA	120
30	CTG!	ACCA!	raa i	AGGA	ACCA	AA A		t Ly:				u Ala				T GCC e Ala -10	172
															TTT Phe		220
35	GTC Val	CAA Gln	GCC Ala 10	GAT Asp	-5 GCC Ala	GCA Ala	CAC His	GCA Ala 15	AAA Lys	GCC Ala	TCA Ser	AGC Ser	TCT Ser 20	5 TTA Leu	GGT Gly	TCT Ser	268
10			GGC					ATC					CGC		AAC Asn		316
15															GCC Ala		364
50															TAC Tyr 70		412
55															TTG Leu	AGC Ser	460
															AGC Ser		508
50	ACC Thr	TCC Ser 105	ATC Ile	GGC Gly	CTC Leu	GGC Gly	GTA Val 110	TTG Leu	ACG Thr	GGC	GTA Val	AGC Ser 115	TAT Tyr	GCC Ala	GTT Val	ACC Thr	556

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	Pro 120	Ası	n Va	l Ası	p Le	Asp 125	Ala	Gl	y Ty	r Arg	130	r As	n Ty	r Il	e Gl	Y Lys 135	604
5	GT( Val	AAC Ası	AC:	r GTC	2 AA/ L Ly: 140	s Asr	GTC Val	CGT	TCC Sei	GGG Gly 145	/ Glu	A CTO	TCO 1 Sea	C GTC r Val	C GG(	C GTG y Val	652
10	CGC	GTC Val	AAA Lys	1 TTC 5 Phe 155	2	ATATO	CGC	CTT	ATTC	rgc #	AAAC	CGCCC	GA GC	CTT	CGCC	3	704
	GII	TIGI	TTT	CTGC	CACC	GC A	ACTA	CACA	AA GC	CGGC	GGT	TIC	TAC	ATA	ATC	CGAAT	764
15	CTG 824 ACA		TTC	TGCC	GCCC	TA I	TTTT	TGAG	G AA	TCCG	AAAT	GŢC	CAA	ACC	ATCA	ATCCAC	,
	תכת	•	٠														83
20	(2)	INF	ORMA	TION	FOR	SEQ	ID	NO: 2	:		•						
25			(i)	(A (B	) LE	CHA NGTH PE: POLO	: 17 amin	4 am c ac	inc		S.						
		(	ii)	MOLE	CULE	TÝP	Ξ: p	rote	in								
		(	xi)	SEQU	ENCE	DES	CRIP'	TION	: SE	C ID	NO:	2:	•				
30	Met -19	Lys											Leu	Pro	Ala -5	Ala	
35	Ala	Leu	Ala	Glu 1	Gly	Ala	Ser	Gly 5	Phe	Tyr	Val	Gln	Ala 10	Asp	Ala	Ala	
	His	Ala 15	Lys	Ala	Ser	Ser	Ser 20	Leu	Gly	Ser	Ala	Lys 25	Gly	Phe	Ser	Pro	
40	Arg 30	Ile	Ser	Ala	Gly	Tyr 35	Arg	Ile	Asn	Asp	Leu 40	Arg	Phe	Ala	Val	Asp 45	
45	Тут	Thr	Arg	Tyr	Lys 50	Asn	Tyr	Lys	Ala	Pro 55	Ser	Thr	Asp	Phe	Lys 60	Leu .	
	Tyr	Ser	Ile	Gly 65	Ala	Ser	Ala	Ile	<b>Tyr</b> 70	Asp	Phe	Asp	Thr	Gln 75	Ser	Pro	
50	Val	Lys	Pro 80	Tyr	Leu	Gly	Ala	Arg 85	Leu	Ser	Leu	Asn	Arg 90	Ala	Ser	Val	
	Asp	Leu 95	Gly	Gly	Ser	Asp	Ser 100	Phe	Ser	Gln	Thr	Ser 105	Ile	Gly	Leu	Gly	
55	Val		Thr	Gly		Ser		Ala	Val	Thr	Pro	Asn	Val	Asp	Leu	Asp	

CCG AAT GTC GAT TTG GAT GCC GGC TAC CGC TAC AAC TAC ATC GGC AAA

Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly Lys Val Asn Thr Val Lys Asn 130 135 140

Val Arg Ser Gly Glu Leu Ser Val Gly Val Arg Val Lys Phe 145 150 155



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10		(ii	) MC	LECU	TLE I	YPE:	DNA	(ge	nomi	c)							
		(iii	.) НҮ	POTH	ETIC	AL:	NO										
15		(iv	) AN	TI-S	ENSE	: NO	•						•				٠
		(vi		A) O	RGAN	ISM:		sser	ia m	enin	giti	dis					
20		(ix		A) N	AME/		CDS	64	3								
25		(1)		A) N	AME/			_pep									
30		(ix		A) N.	AME/			_pep		-		-					
		(xi	) SE	QUEN	CE D	ESCR	IPTI	ON:	SEQ	ID,N	0:3:						
35	GTA:	rctr	GAG (	GCAT	TGAA.	AA T	ATTA	CAAT	G CA	AAAA	GAAA	ATT	TCAG	TAT .	AATA	CGGCAG	60
40	GAT.	ICTT	TAA (	CGGA'	TTCT	TA A	CCAT	ÎTT	C TC	CCTG.	ACCA	TAA	AGGA.	ATC .	AAGA'	T ATG Met -19	118
••	AAA Lys	AAA Lys	GCA Ala	CTT Leu -15	GCC Ala	GCA Ala	CTG Leu	ATT	GCC Ala -10	CTC Leu	GCC Ala	CTC Leu	CCG Pro	GCC Ala -5	GCC Ala	GCA Ala	166
<b>1</b> 5	CTG Leu	GCG Ala	GAA Glu 1	GGC Gly	GCA Ala	TCC Ser	GGC Gly 5	TTT Phe	TAC Tyr	GTC Val	CAA Gln	GCC Ala 10	GAT Asp	GCC Ala	GCA Ala	CAC His	214
50	GCC Ala 15	AAA Lys	GCC Ala	TCA Ser	AGC Ser	TCT Ser 20	TTA Leu	GGT Gly	TCT Ser	GCC Ala	AAA Lys 25	GGC Gly	TTC Phe	AGC Ser	CCG Pro	CGC Arg 30	262
55	ATC Ile	TCC Ser	GCA Ala	GGC Gly	TAC Tyr 35	CGC Arg	ATC Ile	AAC Asn	GAC Asp	CTC Leu 40	Arg	TTC Phe	GCC Ala	GTC Val	GAT Asp 45	TAC Tyr	310
60	ACG Thr	CGC Arg	TAC Tyr	AAA Lys 50	AAC Asn	TAT Tyr	AAA Lys	CAA Gln	GTC Val 55	CCA Pro	TCC Ser	ACC Thr	GAT Asp	TTC Phe 60	AAA Lys	CTT Leu	358
	TAC Tyr	AGC Ser	ATC Ile 65	GGC Gly	GCG Ala	TCC Ser	GCC Ala	ATT Ile 70	TAC Tyr	GAC Asp	TTC Phe	GAC Asp	ACC Thr 75	CAA Gln	TCC Ser	CCC Pro	406

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5			Pro					Arg	TTG Leu				Arg				454
J	GAC Asp 95	Phe	AAC Asn	GGC	AGC Ser	GAC Asp 100	AGC Ser	TTC Phe	AGC Ser	CAA Gln	ACC Thr 105	TCC Ser	ACC	GGC Gly	CTC Leu	GGC Gly 110	502
10	GTA Val	TTG Leu	GCG Ala	GGC Gly	GTA Val 115	AGC Ser	TAT Tyr	GCC Ala	GTT Val	ACC Thr 120	CCG Pro	AAT Asn	GTC Val	GAT Asp	TTG Leu 125	GAT Asp	550
15	GCC Ala	GGC Gly	TAC Tyr	CGC Arg 130	TAC Tyr	AAC Asn	TAC Tyr	ATC Ile	GGC Gly 135	AAA Lys	GTC Val	AAC Asn	ACT Thr	GTC Val 140	AAA Lys	AAT Asn	598
20	GTC Val	CGT Arg	TCC Ser 145	GGC Gly	GAA Glu	CTG Leu	TCC Ser	GCC Ala 150	GGC Gly	GTA Val	CGC Arg	GTC Val	AAA Lys 155	TTC Phe	TGA	TATACGO	650
	GTT	ATTC:	EGC A	AAAC	GCCC	GA GC	CIT	rcgg	GGT	TTTT	TTT	TCCC	CCG	cc c	CAACT	TACACA	71C
25	(2)	INF	ORMAT	CION	FOR	SEQ	ID N	NO : 4 :	<b>!</b>								
30			(i) S	(A)		IGTH: PE: a	: 179 umino	ami aci			<b>i</b>						
		( i	li) M	OLEC	ULE	TYPE	: pr	otei	n	•							
35		()	(i) S	EQUE	NCE	DESC	RIPI	ION:	SEC	) ID	NO : 4	:					
	Met -19	Lys	Lys	Ala	Leu -15	Ala	Ala	Leu	Ile	Ala -10	Leu	Ala	Leu	Pro	Ala -5	Ala	•
40	Ala	Leu	Ala	Glu 1	Gly	Ala	Ser	Gly 5	Phe	Tyr	Val	Gln	Ala 10	Asp	Ala	Ala	•
45	His	Ala 15	Lys	Ala	Ser	Ser	Ser 20	Leu	Gly	Ser	Ala	Lys 25	Gly	Phe	Ser	Pro	
	Arg 30	<b>ļle</b>	Ser	Ala	Gly	Tyr 35	Arg	Ile	Asn		Leu 40	Arg	Phe	Ala	Val	Asp 45	
50	Tyr	Thr	Arg	Tyr	Lys 50	Asn	Тут	Lys	Gln	<b>Val</b> 55	Pro	Ser	Thr	Asp	Phe 60	Lys	
	Leu	Тут	Ser	Ile 65	Gly	Ala	Ser	Ala	Ile 70	Tyr	Asp	Phe	Asp	Thr 75	Gln	Ser	
55	Pro	Val	Lys 80	Pro	Туг	Leu	Gly	Ala 85	Arg	Leu ´	Ser	Leu .	Asn 90	Arg	Ala	Ser	
<b>40</b>	Val	Asp 95	Phe	Asn	Gly		Asp 100	Ser	Phe	Ser		Thr 105	Ser '	Thr	Gly :	Leu	

Gly Val Leu Ala Gly Val Ser Tyr Ala Val Thr Pro Asn Val Asp Leu 110 115 120 120

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Asp	Ala	Gly	Tyr	Arg	Tyr	Asn	Tyr	Ile	Gly	Lys	Val	Asn	Thr	Val	Lys
				130					135					140	

Asn Val Arg Ser Gly Glu Leu Ser Ala Gly Val Arg Val Lys Phe 150

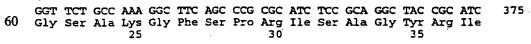
WO 96/29412

	(2) INFO	RMATION FOR SEQ ID NO:5:
10	, <b>(i)</b>	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 850 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear
15 .	(ii)	MOLECULE TYPE: DNA (genomic)
	(iii)	HYPOTHETICAL: NO
20	(iv)	ANTI-SENSE: NO
2.5	(vi)	ORIGINAL SOURCE: (A) ORGANISM: Neisseria meningitidi (B) STRAIN: 24063
25	(ix)	FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 208732
30	(ix)	FEATURE: (A) NAME/KEY: sig_peptide (B) LOCATION: 208264
35	(ix)	FEATURE: (A) NAME/KEY: mat_peptide (B) LOCATION: 265732

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5: 40

TTGCCGTCGG CAAAGCAGCC GGATACCGCT ACGTATCTTG AAGTATTAAA AATATTACGA 120 TGCAAAAAGA AAATTTAAGT ATAATAAAGC AGAATTCTIT AACGGATTCT TAACAATTTT 180 TCTAACTGAC CATAAAGGAA CCAAAAT ATG AAA AAA GCA CTT GCC ACA CTG Met Lys Lys Ala Leu Ala Thr Leu -19 50 ATT GCC CTC GCT CTC CCG GCC GCC GCA CTG GCG GAA GGC GCA TCC GGC Ile Ala Leu Ala Leu Pro Ala Ala Ala Leu Ala Glu Gly Ala Ser Gly -10 TTT TAC GTC CAA GCC GAT GCC GCA CAC GCA AAA GCC TCA AGC TCT TTA Phe Tyr Val Gln Ala Asp Ala Ala His Ala Lys Ala Ser Ser Ser Leu 327

CACCCATCCG CCGCGTGATG CCGCCACCAC CATTTAAAGG CAACGCGCGG GTTAACGGCT





	AAC Asn	GAC Asp	CTC Leu 40	CGC Arg	TTC Phe	GCC Ala	GTC Val	GAT Asp 45	TAC Tyr	ACG Thr	CGC Arg	TAC Tyr	AAA Lys 50	AAC Asn	TAT Tyr	AAA Lys	423
5									TAC Tyr								471
10									GTC Val								519
15									GAC Asp								567
20									GTA Val 110							GCC Ala	615
20									GCC Ala								663
25									GTC Val								711
30		GTG Val					TGAT	TATGO	CGC (	TATT	TTCTO	EC A#	ACC	CCGA			759
	GCCI	TCGC	CG G	TTT	GTT	T CI	GCC#	CCGC	AAC	TAÇA	CAA	GCCG	GCGG	TT 1	TGTA	CGATA	819
35	ATCC	CGA	TG C	TGC	GCTT	rc ro	CCGC	CCT	À Ť								850
40	(2)							10:6:	: rics:								
				(B)	TYE	E: a	mino	ami aci inea		cids	;						
45		(i	.i) M	OLEC	TULE	TYPE	: pr	otei	n								
		()	ci) S	EQUI	ENCE	DESC	RIPT	: NOI	SEC	] ID	NO: 6	i :				•	
50	Met -19	Lys	Lys	Ala	Leu -15	Ala	Thr	Leu	Ile	Ala -10	Leu	Ala	Leu	Pro	Ala -5	Ala	
	Ala	Leu	Ala	Glu 1	Gly	Ala	Ser	Gly 5	Phe	Tyr	Val	Gln	Ala 10	Asp	Ala	Ala	
55				1				5	Phe Gly				10				
55 60	His	Ala 15	Lys	1 Ala	Ser	Ser	Ser 20	5 Leu		Ser	Ala	Lys 25	10 Gly	Phe	Ser	Pro	

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Color Color II and the second Color

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	Tyr	Ser	Ile	Gly 65	Ala	Ser	Ala	Ile	Tyr 70	Asp	Phe	Asp	Thr	Gln 75	Ser	Pro	
5	Val	Lys	Pro 80	Тут	Leu	Gly	Ala	Arg 85	Leu	Ser	Leu	Asn	Arg 90	Ala	Ser	Val	
	Asp	Leu 95	Gly	Gly	Ser	Asp	Ser 100	Phe	Ser	Gln	Thr	Ser 105	Thr	Gly	Leu	Gly	
10	Val 110	Leu	Ala	Gly	Val	Ser 115	Tyr	Ala	Val	Thr	Pro 120	Asn	Val	Asp	Leu	<b>Asp</b> 125	
15	Ala	Gly	Tyr	Arg	Tyr 130	Asn	Tyr	Ile	Gly	Lys 135	Val	Asn	Thr	Val	Lys 140	Asn	
13	Val	Arg	Ser	Gly 145	Glu	Leu	Ser	Ala	Gly 150	Val	Arg	Val	Lys	Phe 155			
20	(2)	INFO	ORMA!	rion	FOR	SEQ	ID N	10:7:									
25		(i)	() ()	A) LI B) TY C) SI	ENGTH (PE:	nucl	lO ba leic ESS:	ISTIC ase p acid doub ar	airs !	i .							
		(ii)	MOI	LECUI	LE TY	PE:	DNA	(gen	omic	:)							
30		(iii) (iv)			ETICA ENSE:		10										
35			ORI	(GINA	AL SC	URCI	Neis	sseri	a go	nori	hoea	ıe					
40		(ix)	(2		ME/F			765	<b>.</b>						-		
45		(ix)	(2		ME/F			_pept				,					
		(ix)	(2		ME/F			_pept									
50		(xi)	SE(	QUENC	E DE	SCR	PTI	ON: S	EQ I	D NO	):7:						
	CCC	GCC1	er (	GCGG		רד כנ	CAAAC	CCGTT	TGO	CAAGT	TTC	ACC	CATCO	GC (	GCG1	GATGC	60
55	CGC	GTT	CAA (	GGC2	AACGC	G CC	GGT.	TAACG	GAT	rtigo	CGT	CGG	CAAAG	CA C	CCGC	SATGCC	120
	GCC	GCGT?	ATC :	ÍTGA(	GCA1	T G	AAA!	TATTA	CG/	ATGC	AAAA	AGA	LTAAL	TC A	GTAI	TAATAC	180
	GGC	AGGAT	rrc :	TTA	ACGG!	TI	ATTA	ACAAI	r TT	TCT	CCT	GAC	ATA	AG (	AACC	TAAAAT	240

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ATG AAA AAA GCA CTT GCC GCA CTG ATT GCC CTC GCA CTC CCG GCC GCC Met Lys Lys Ala Leu Ala Ala Leu Ile Ala Leu Ala Leu Pro Ala Ala

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5												CAA Gln				33(
J												AAA Lys 25				384
10												CGC Arg				432
15												ÀCC Thr				480
20												GAC Asp				528
25												AAC Asn				57€
												TCC Ser 105				624
30												AAT Asn				672
35												AAC Asn				720
40												GTC Val		TGAT	'ATACGO	77
	GTTA	TTCC	GC A	AACC	GCCG	A GC	CTTC	:GGCG	GII	1111	.c					810

- (2) INFORMATION FOR SEQ ID NO:8:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 174 amino acids
      (B) TYPE: amino acid
- 50 (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8: 55
  - Met Lys Lys Ala Leu Ala Ala Leu Ile Ala Leu Ala Leu Pro Ala Ala
- Ala Leu Ala Glu Gly Ala Ser Gly Phe Tyr Val Gln Ala Asp Ala Ala 1 5 60
  - His Ala Lys Ala Ser Ser Ser Leu Gly Ser Ala Lys Gly Phe Ser Pro

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	Arg 30	Ile	Ser	Ala	Gly	Tyr 35	Arg	Ile	Asn	Asp	Leu 40	Arg	Phe	Ala	Val	Asp 45	
5	Tyr	Thr	Arg	Tyr	Lys 50	Asn	Tyr	Lys	Ala	Pro 55	Ser	Thr	Asp	Phe	Lys 60	Leu	
10	Tyr	Ser	Ile	Gly 65	Ala	Ser	Val	Ile	Tyr 70	Asp	Phe	Asp	Thr	Gln 75	Ser	Pro	
10	Val	Lys	Pro 80		Phe	Gly	Ala	Arg 85	Leu	Ser	Leu	Asn	Arg 90	Ala	Ser	Ala	
15	His	Leu 95	Gly	Gly	Ser		Ser 100	Phe	Ser	Lys	Thr	Ser 105	Ala	Gly	Leu	Gly	
	Val 110	Leu	Ala	Gly	Val	Ser 115	Tyr	Ala	Val	Thr	Pro 120	Asn	Val	Asp	Leu	Asp 125	
20	Ala	Gly	Tyr	Arg	ፒኒፕ 130	Asn	Tyr	Val	Gly	Lys 135	Val	Asn	Thr	Val	Lys 140	Asn	
25	Val	Arg	Ser	Gly 145		Leu	Ser	Ala	Gly 150	Val	Arg	Val	Lys	Phe 155			
	(2)							10:9:					•				
30		(i)	( <i>I</i>	A) LI 3) T	ENGTI (PE:	i: 16 amir				5							
35			ORI	IGINZ	AL SO	URCE	Neis	sser:	ia me	, ening	gitio	lis					
40																,	
		(xi)	SE(	OUEN	CE DI	ESCR	PTI	ON: 5	SEQ I	D NO	0:9:						
45		Met 1	t Ly:	s Ly:	s Ala	Let 5	ı Ala	a Thi	r Lei	ı Ile	≥ Ala 10	a Leu	ı Ala	i Lei	ı Pro	Ala 15	Ala
	(2)	INF	ORMA!	rion	FOR	SEQ	ID 1	NO:10	0:								
50		(i)	(1	A) LI B) T	ENGTI YPE :	i: 1: amin				5							
55		(ii	) MO	LECUI	LE T	PE:	pro	tein			•						
		(vi		A) 0	RGAN:		Nei:	sser	ia m	ening	gitio	iis					



	(XI	) SEC	UENCE	, DESCR	IPIIO	M: DE/	ז עד נ	MO: 10:						
5		Leu 1	Ala	Leu Pr	o Ala 5	Ala'	Ala Le	eu Ala	Glu 10	Gly	Ala	Ser	Gly	Phe 15
,	(Ź)	INFO	RMATI	ON FOR	SEQ	ID NO:	:11:	_						
10		(i)	(A)	ENCE C LENGT TYPE: TOPOL	H: 15 amin	amino o acio	ació	ls						
		(ii)	MOLE	CULE T	YPE: 1	protei	.n							
15 .		(vi)	(A)	INAL SO ORGANI STRAII	ISM: 1	Neisse	eria m	ening	itid	is		•		
20														
		(xi)	SEQU	ENCE DI	ESCRI	PTION:	SEQ	ID NO	:11:					
25		Gly 1	Ala :	Ser Gly	Phe 5	Tyr V	al Gl	n Ala	Asp 10	Ala	Ala	His	Ala	Lys 15
	(2)	INFO	RMATI	ON FOR	SEQ 1	ID NO:	12:			•				
30		(i)	(A) (B)	ENCE CH LENGTH TYPE: TOPOLO	l: 15 amino	amino acid	acid	s		~				
	* 1	(ii)	MOLE	TULE TY	PE: p	protei	n	,						
35		(vi)	(A)	NAL SO ORGANI STRAIN	SM: N	Veisse	ria m	ening	itidi	is				
40														
40		(xi)	SEQUE	ENCE DE	SCRIF	TION:	SEQ :	D NO	:12:					
45		Ala 1	Ala I	lis Ála	Lys 5	Ala S	er Se	r Ser	Leu 10	Gly	Ser	Ala	Lys	Gly 15
70	(2)	INFOR	OITAMS	N FOR	SEQ I	D NO:	13:			,				
50		(i)	(A) (B)	NCE CH LENGTH TYPE: TOPOLO	: 15 amino	amino acid	acid	5						
		(ii)	MOLEC	ULE TY	PE: p	rotei	n							
55		(vi)	(A)	NAL SO ORGANI STRAIN	SM: N	eisse:	ria me	eningi	tidi	.s	es.			

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	(xi	) SEQ	UENCI	DES	CRIP	TION	i: SI	EQ II	ои с	:13:							
5		Gly 1	Ser	Ala		Gly 5	Phe	Ser	Pro	Arg	Ile 10	Ser	Ala	Gly	Tyr	Arg 15	
3	(2)	INFO	RMATI	ON F	OR S	EQ I	D NC	:14	:								
10		(i)	(A) (B)	LENCE TYP TOP	GTH: E: a	15 mino	amir aci	o ac					÷				
		(ii)	MOLE	CULE	TYP	E: p	rote	in									
15	-	(vi)	(A)	INAL ORG STR	ANIS	M: N	leiss	eria	a mei	ning:	itid:	is					
20																	
-0		(xi)	SEQU	JENCE	DES	CRIP	OIT	i: SI	EQ II	ON O	:14:						
25		Ser 1	Ala	GJA ,	Tyr .	Arg 5	Ile	Asn	Asp	Leu	Arg 10	P'ne	Ala	Val	Asp	T,T 15	
-3	(2)	INFÒ	RMATI	ON F	OR S	EQ I	D NO	:15	:				,				
30		(±)	(A)	LENCE LENC TYP: TOP	GTH: E: a	16 mino	amin aci	o ao .d									
	• •	(ii)	MOLE	CULE	TYP	E: p	rote	in									
35		(vi)	(A)	INAL ORG STR	ANIS	M: N	leiss	eria	a mei	ning:	itid:	is					٠
40																	
		(xi)	SEQU	JENCE	DES	CRIF	OIT	1: S	EQ II	D NO	:15:						
45		Phe 1	Ala	Val .	Asp	Tyr 5	Thr	Arg	Tyr	Lys	Asn 10	Týr	Lys	Ala	Pro	Ser 15	Thr
	(2)	INFO	RMAT]	ON F	OR S	EQ I	D NO	:16	•								
50		(i)	(A)	JENCE LEN TYP TOP	GTH: E: a	15 mino	amir aci	o a		:			-			-	
55		(ii)	MOLI	CULE	TYP	E: p	rote	ein					•				

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Neisseria meningitidis
 (B) STRAIN: 608B

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(xi)	SECTIENCE	DESCRIPTION:	SEO	ID	NO-16
( ** )	SECULIACE	DEGCETT TION.		10	MOLIU

Tyr Lys Ala Pro Ser Thr Asp Phe Lys Leu Tyr Ser Ile Gly Ala

5 (2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 amino acids
- 10 (B) TYPE: amino acid (D) TOPOLOGY: linear

  - (ii) MOLECULE TYPE: protein
- 15 (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Neisseria meningitidis
  - (B) STRAIN: 608B

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Tyr Ser Ile Gly Ala Ser Ala Ile Tyr Asp Phe Asp Thr Gln Ser 10

25 (2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid (D) TOPOLOGY: linear

  - (ii) MOLECULE TYPE: protein
- 35 (vi) ORIGINAL SOURCE:

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- (A) ORGANISM: Neisseria meningitidis
- (B) STRAIN: 608B
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Phe Asp Thr Gln Ser Pro Val Lys Pro Tyr Leu Gly Ala Arg Leu

- (2) INFORMATION FOR SEQ ID NO:19:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
- 50 (D) TOPOLOGY: linear.
  - (ii) MOLECULE TYPE: protein
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: Neisseria meningitidis
      - (B) STRAIN: 608B
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19: 60
- Leu Gly Ala Arg Leu Ser Leu Asn Arg Ala Ser Val Asp Leu Gly 10

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(2)	INFORMATION	FOR	SEO	ID	NO:20:
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(i) SEQ	UENCE	CHARACTERISTICS:
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- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
- 10 (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Neisseria meningitidis
  - (B) STRAIN: 608B
- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ser Val Asp Leu Gly Gly Ser Asp Ser Phe Ser Gln Thr Ser Ile 10

- 20 (2) INFORMATION FOR SEQ ID NO:21:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid (D) TOPOLOGY: linear 25
  - (ii) MOLECULE TYPE: protein
  - (vi) ORIGINAL SOURCE:
- 30 (A) ORGANISM: Neisseria meningitidis
  - (B) STRAIN: 608B
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21: 35

Ser Gln Thr Ser Ile Gly Leu Gly Val Leu Thr Gly Val Ser Tyr

- (2) INFORMATION FOR SEQ ID NO:22: 40
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 amino acids
    (B) TYPE: amino acid
- (D) TOPOLOGY: linear 45
- (ii) MOLECULE TYPE: protein
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: Neisseria meningitidis
- 50 (B) STRAIN: 608B
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22: 55
- Thr Gly Val Ser Tyr Ala Val Thr Pro Asn Val Asp Leu Asp Ala

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121	INFORMATION	FOR	CEO	TD	NO. 23
(2)	INFORMATION	FUR	SEU	עב	NO: 23

(I) SECOMICE CHARACTERIZATION	(i	) SECUENCE	CHARACTERISTICS
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- (A) LENGTH: 15 amino acids (B) TYPE: amino acid
- (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
- 10 (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Neisseria meningitidis
  - (B) STRAIN: 608B

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Val Asp Leu Asp Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly Lys Val

20 (2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 amino acids
- 25 (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: protein
- 30 (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Neisseria meningitidis
  - (B) STRAIN: 608B

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

> Tyr Ile Gly Lys Val Asn Thr Val Lys Asn Val Arg Ser Gly Glu 5 10

40 (2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
- 50 (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Neisseria meningitidis (B) STRAIN: 608B

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Val Arg Ser Gly Glu Leu Ser Val Gly Val Arg Val Lys Phe

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(i)	SEQUENCE	CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: amino acid (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Neisseria meningitidis (B) STRAIN: 608B

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Phe Ala Val Asp Tyr Thr Arg Tyr Lys Asn Tyr Lys Ala Pro Ser Thr 1 10 15

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Asp Phe Lys Leu Tyr Ser Ile Gly Ala 20

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